Please replace the paragraph beginning at page 7, lines 3-21 with the following rewritten paragraph:

A2

Figures 8A and 8B illustrate fluorescence images of oligonucleotide arrays monitoring 1,650 genes in parallel (1 of a set of 4 arrays covering 6,600 genes). In Fig. 8A representative hybridization patterns of fluorescently labeled cRNA from normal (HT-125) and malignant breast (BT-474) cells are shown. The images were obtained after hybridization of arrays with fragmented, biotin labeled cRNA and subsequent staining with a phycoerytherin-strepavidin conjugate. Bright rows indicate messages present at high levels. Low level messages (1-10 copies/cell) are unambiguously detected based on quantitative analysis of PM/MM intensity patterns. In the lower portion of the Figure a magnified view of a portion of the array highlighting examples of altered gene expression between BT-474 and HT-125 is shown. In area 1, induced (>10-fold change in hybridization intensity) genes are shown, in area 2, unchanged (<2-fold change in hybridization intensity) are shown, and in area 3 repressed (>10-fold change in hybridization intensity) are shown. Fig. 8B illustrates zoom-in images of genes 1, 2, & 3 in (A) as 20 probe pairs of perfect-matched (PM) and single base mis-matched (MM) oligonucleotide probe cells. Average fluorescence intensity difference for PM-MM in HT-125 versus BT-474 (normalized to β-Actin and GAPDH signals) are shown in the three rows. In row 1 (Her2/neu oncogene) the average intensities are 111 versus 5,127; in row 2 (laminin receptor) 3,495 versus 6,088; and in row 3 (galectin-1) 7,952 versus undetected.

Please replace the paragraph beginning at page 7, lines 22-26 with the following rewritten paragraph:

A3

Figure 9 illustrates expression profiles of subset of genes from normal versus malignant breast cells. Average perfect match-mismatch (PM-MM) intensity differences (normalized to β-Actin and GAPDH signals) were plotted for the genes highlighted in Figure 8A that demonstrated greater than a 2-fold difference in hybridization signals between HT-125 and BT-474. Values for signals off scale are indicated.

Please replace the paragraph beginning at page 7, lines 27-32 with the following rewritten paragraph:

A4

Figure 10 illustrates p53 sequence analysis and mutation detection by hybridization. In Figure 10A, an image of the p53 genotyping array hybridized to 1,490 bp of the BT-474 breast carcinoma p53 gene (left) is shown. A zoom-in view of hybridization patterns of p53 wild-type reference and BT-474 DNA in a region of a G→A single-base mutation in BT-474 is shown at the right. In each column are 4 identical probes with an A, C, G or

Please replace the paragraph beginning at page 8, lines 1-12 with the following rewritten paragraph:

A5

T substituted at a central position. The hybridized target sequence identified based on mismatch detection from left to right as the complement of the substitution base with the brightest signal. The G→A transition seen in BT-474 is accompanied by a loss of signal at flanking positions as these probes now have a single-base mismatch to the target distinct from the query position. Fig. 10B (top),

comparison of wild-type reference (black) and BT-474 p53 gene (red) hybridization intensity patterns from sense (above) and anti-sense strands (below) in the region containing a mutation. The area shown demonstrates the "footprint" and detection of a single-base difference between the samples (vertical green line). GeneChip data analysis output is shown (bottom) that unambiguously identifies a G→A base change at nucleotide 1,279 of p53 in BT-474 resulting in a glutamic acid to lysine amino acid change in exon 8 (DNA binding domain). The upper portion of output displays the p53 wild-type reference sequence. Aligned outputs of wild-type p53 control and BT-474 samples are shown.

Please replace the paragraph beginning at page 52, lines 10-20 with the following rewritten paragraph:

Figure 8A (top panel) shows representative hybridization patterns of total message from normal and malignant breast cells to sets of 20 probe pairs from 1,650 gene sequences (one array of a set of 4 encompassing 6,600 human genes). Clear examples of unchanged and altered patterns of gene expression can be observed by visual comparison of the fluorescence intensities of probes sets from these two samples. The quantitative analysis of hybridization patterns is based on the assumption that for a specific mRNA the perfect-matched (PM) probes will hybridize more strongly on average than their mis-matched (MM) partners (Fig. 8B). The average difference in intensity between PM and MM hybridization signals is computed together with the average of the logarithm of the PM/MM ratios for each probe set. These values are then used to determine the relative copy number of a detected message.

Please replace the paragraph beginning at page 53, lines 1-4 with the following rewritten paragraph:

A7

hybridization signal intensities, that range over 4-orders of magnitude, revealed all categories of message expression changes including repressed (>10-fold down), down-regulated (<10-fold down), up-regulated (<10-fold up) and induced (>10-fold up) mRNAs between normal and malignant cells as shown in Fig. 9.

Please replace the paragraph beginning at page 53, lines 5-13 with the following rewritten paragraph:

A8

Genes that are repressed and induced/activated may provide a particularly good starting point to decipher the molecular pathways involved in programs of tumorigenesis. To identify the genes falling into each of these two categories we sorted the normal and malignant message populations to identify those genes that demonstrated a 10-fold or greater difference in messages intensities. This analysis revealed 168 genes repressed and 137 genes activated in BT-474 when compared to HT-125, as shown in Table 3 (Figure 10). 260 of the messages displaying differential expression corresponded to GenBank human full length genes, 45 to ESTs with homologies to other eukaryotic or viral genes.

IN THE CLAIMS:

Please cancel claims 33, 38, 41-43 without prejudice or disclaimer.